

Supplementary Figure S1. (A) Distribution of homoplasy across individual characters in all simulated data sets used in the study (homoplasy calculated as (1/cCI – 1) and represents extra number of steps for each individual character). (B) Area plot showing percentage of individual characters across all simulated data sets with cCI = 1 (green field) and cCI < 1 (grey field).

A picture containing writing implement, stationary, pencil

Description automatically generated

Supplementary Figure S2. Results of rank tests for nRF, nMS, and KF tree comparison metrics. Stacked bars show how frequently each program was scored at each rank.

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| Supplementary Table S1: Normalized RF (uniform) by number of taxa (median values) | | | | | | | | | | | | |
|  | 0% missing data | | | | 20% missing data | | | | 50% missing data | | | | |
| Taxa | IQ-Tree | RAxML | MrBayes | RevBayes | IQ-Tree | RAxML | MrBayes | RevBayes | IQ-Tree | RAxML | MrBayes | RevBayes | |
| 50 | 0.320 | 0.267 | 0.230 | 0.219 | 0.416 | 0.331 | 0.288 | 0.294 | 0.683 | 0.448 | 0.438 | 0.432 | |
| 100 | 0.369 | 0.276 | 0.222 | 0.235 | 0.408 | 0.344 | 0.287 | 0.284 | 0.661 | 0.454 | 0.413 | 0.398 | |
| 150 | 0.266 | 0.232 | 0.186 | 0.201 | 0.300 | 0.281 | 0.226 | 0.242 | 0.517 | 0.415 | 0.366 | 0.356 | |
| 200 | 0.216 | 0.230 | 0.161 | 0.175 | 0.272 | 0.271 | 0.206 | 0.213 | 0.439 | 0.384 | 0.323 | 0.328 | |
| 250 | 0.166 | 0.235 | 0.132 | 0.148 | 0.211 | 0.271 | 0.173 | 0.176 | 0.383 | 0.364 | 0.291 | 0.289 | |
| 300 | 0.227 | 0.228 | 0.161 | 0.171 | 0.285 | 0.272 | 0.207 | 0.180 | 0.470 | 0.388 | 0.336 | 0.343 | |
| 350 | 0.226 | 0.222 | 0.158 | 0.162 | 0.275 | 0.278 | 0.204 | 0.205 | 0.453 | 0.394 | 0.321 | 0.323 | |
| 400 | 0.202 | 0.227 | 0.152 | 0.159 | 0.265 | 0.275 | 0.195 | 0.192 | 0.446 | 0.380 | 0.319 | 0.318 | |
| 450 | 0.143 | 0.190 | 0.109 | 0.120 | 0.185 | 0.231 | 0.139 | 0.138 | 0.311 | 0.323 | 0.245 | 0.250 | |
| 500 | 0.147 | 0.170 | 0.110 | 0.119 | 0.180 | 0.207 | 0.144 | 0.146 | 0.322 | 0.321 | 0.255 | 0.244 | |

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| Supplementary Table S2: Normalized MS (uniform) by number of taxa (median values) | | | | | | | | | | | | |
|  | 0% missing data | | | | 20% missing data | | | | 50% missing data | | | | |
| Taxa | IQ-Tree | RAxML | MrBayes | RevBayes | IQ-Tree | RAxML | MrBayes | RevBayes | IQ-Tree | RAxML | MrBayes | RevBayes | |
| 50 | 0.176 | 0.319 | 0.204 | 0.231 | 0.216 | 0.411 | 0.230 | 0.248 | 0.297 | 0.541 | 0.425 | 0.468 | |
| 100 | 0.139 | 0.305 | 0.175 | 0.179 | 0.150 | 0.331 | 0.193 | 0.200 | 0.190 | 0.429 | 0.284 | 0.296 | |
| 150 | 0.073 | 0.192 | 0.112 | 0.159 | 0.078 | 0.197 | 0.118 | 0.172 | 0.113 | 0.292 | 0.178 | 0.175 | |
| 200 | 0.069 | 0.200 | 0.084 | 0.118 | 0.070 | 0.203 | 0.092 | 0.128 | 0.098 | 0.252 | 0.125 | 0.137 | |
| 250 | 0.047 | 0.213 | 0.066 | 0.106 | 0.050 | 0.213 | 0.076 | 0.084 | 0.074 | 0.257 | 0.102 | 0.107 | |
| 300 | 0.072 | 0.209 | 0.093 | 0.145 | 0.078 | 0.217 | 0.112 | 0.142 | 0.095 | 0.261 | 0.140 | 0.169 | |
| 350 | 0.051 | 0.161 | 0.076 | 0.087 | 0.050 | 0.172 | 0.080 | 0.083 | 0.073 | 0.203 | 0.105 | 0.119 | |
| 400 | 0.052 | 0.171 | 0.079 | 0.097 | 0.055 | 0.181 | 0.082 | 0.082 | 0.074 | 0.224 | 0.102 | 0.115 | |
| 450 | 0.039 | 0.149 | 0.046 | 0.090 | 0.044 | 0.154 | 0.052 | 0.050 | 0.053 | 0.177 | 0.061 | 0.084 | |
| 500 | 0.035 | 0.123 | 0.047 | 0.089 | 0.039 | 0.124 | 0.050 | 0.054 | 0.051 | 0.151 | 0.062 | 0.069 | |

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| Supplementary Table 3: Normalized RF (uniform) by number of taxa (STDEV.S values) | | | | | | | | | | | | |
|  | 0% | | | | 20% | | | | 50% | | | |
| Taxa | IQ-Tree | RAxML | MrBayes | RevBayes | IQ-Tree | RAxML | MrBayes | RevBayes | IQ-Tree | RAxML | MrBayes | RevBayes |
| 50 | 0.077 | 0.047 | 0.045 | 0.047 | 0.097 | 0.042 | 0.062 | 0.063 | 0.086 | 0.029 | 0.025 | 0.020 |
| 100 | 0.051 | 0.022 | 0.025 | 0.027 | 0.045 | 0.017 | 0.022 | 0.019 | 0.055 | 0.019 | 0.028 | 0.029 |
| 150 | 0.030 | 0.013 | 0.014 | 0.020 | 0.041 | 0.019 | 0.021 | 0.019 | 0.055 | 0.021 | 0.026 | 0.023 |
| 200 | 0.024 | 0.013 | 0.017 | 0.014 | 0.025 | 0.012 | 0.021 | 0.021 | 0.033 | 0.016 | 0.012 | 0.011 |
| 250 | 0.022 | 0.018 | 0.008 | 0.012 | 0.034 | 0.013 | 0.016 | 0.021 | 0.034 | 0.017 | 0.020 | 0.018 |
| 300 | 0.024 | 0.015 | 0.009 | 0.008 | 0.023 | 0.014 | 0.021 | 0.010 | 0.018 | 0.017 | 0.013 | 0.009 |
| 350 | 0.021 | 0.020 | 0.012 | 0.012 | 0.013 | 0.016 | 0.011 | 0.012 | 0.026 | 0.014 | 0.016 | 0.011 |
| 400 | 0.019 | 0.014 | 0.012 | 0.015 | 0.018 | 0.011 | 0.014 | 0.014 | 0.019 | 0.015 | 0.009 | 0.022 |
| 450 | 0.006 | 0.012 | 0.008 | 0.011 | 0.019 | 0.017 | 0.012 | 0.014 | 0.026 | 0.013 | 0.017 | 0.019 |
| 500 | 0.014 | 0.004 | 0.006 | 0.005 | 0.016 | 0.007 | 0.006 | 0.008 | 0.013 | 0.008 | 0.009 | 0.056 |

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| Supplementary Table S4: Normalized MS (uniform) by number of taxa (STDEV.S values) | | | | | | | | | | | | |
|  | 0% missing data | | | | 20% missing data | | | | 50% missing data | | | |
| Taxa | IQ-Tree | RAxML | MrBayes | RevBayes | IQ-Tree | RAxML | MrBayes | RevBayes | IQ-Tree | RAxML | MrBayes | RevBayes |
| 50 | 0.032 | 0.087 | 0.062 | 0.063 | 0.039 | 0.075 | 0.081 | 0.092 | 0.064 | 0.016 | 0.055 | 0.056 |
| 100 | 0.047 | 0.031 | 0.012 | 0.012 | 0.029 | 0.020 | 0.024 | 0.027 | 0.043 | 0.029 | 0.032 | 0.044 |
| 150 | 0.023 | 0.031 | 0.019 | 0.043 | 0.024 | 0.033 | 0.018 | 0.026 | 0.023 | 0.023 | 0.032 | 0.032 |
| 200 | 0.018 | 0.025 | 0.016 | 0.032 | 0.020 | 0.029 | 0.015 | 0.035 | 0.023 | 0.025 | 0.020 | 0.020 |
| 250 | 0.008 | 0.012 | 0.014 | 0.025 | 0.010 | 0.016 | 0.014 | 0.018 | 0.008 | 0.017 | 0.013 | 0.011 |
| 300 | 0.011 | 0.025 | 0.015 | 0.029 | 0.015 | 0.026 | 0.012 | 0.019 | 0.012 | 0.021 | 0.013 | 0.022 |
| 350 | 0.008 | 0.017 | 0.008 | 0.009 | 0.009 | 0.016 | 0.009 | 0.007 | 0.009 | 0.013 | 0.010 | 0.012 |
| 400 | 0.009 | 0.016 | 0.011 | 0.015 | 0.010 | 0.017 | 0.011 | 0.009 | 0.010 | 0.012 | 0.012 | 0.016 |
| 450 | 0.006 | 0.019 | 0.011 | 0.022 | 0.007 | 0.017 | 0.012 | 0.011 | 0.006 | 0.012 | 0.015 | 0.018 |
| 500 | 0.008 | 0.012 | 0.007 | 0.017 | 0.007 | 0.015 | 0.008 | 0.010 | 0.007 | 0.010 | 0.006 | 0.023 |

Supplementary Table S5: Results of the rank test using the nRF values for each data set replicate. Phylogenetic inference programs were ranked from the best (1st rank) to the worst performing (4th rank) based on the accuracy of the reconstructed topologies. Numbers indicate percentage of the total number of analyses in which programs scored at each rank.

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|  | **0% missing data** | | | | **20% missing data** | | | | **50% missing data** | | | |
| **1** | **2** | **3** | **4** | **1** | **2** | **3** | **4** | **1** | **2** | **3** | **4** |
| MrBayes | 85 | 12 | 2 | 1 | 52 | 44 | 3 | 1 | 47 | 52 | 1 | 0 |
| RevBayes | 14 | 84 | 2 | 0 | 47 | 51 | 2 | 0 | 52 | 46 | 2 | 0 |
| IQ-TREE | 1 | 2 | 58 | 39 | 0 | 2 | 48 | 50 | 0 | 0 | 16 | 84 |
| RAxML | 0 | 2 | 38 | 60 | 1 | 3 | 47 | 49 | 1 | 2 | 81 | 16 |

Supplementary Table S6: Results of the rank test using the nMS values for each data set replicate. Phylogenetic inference programs were ranked from the best (1st rank) to the worst performing (4th rank) based on the accuracy of the reconstructed topologies. Numbers indicate percentage of the total number of analyses in which programs scored at each rank.

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|  | **0% missing data** | | | | **20% missing data** | | | | **50% missing data** | | | |
| **1** | **2** | **3** | **4** | **1** | **2** | **3** | **4** | **1** | **2** | **3** | **4** |
| MrBayes | 13 | 83 | 4 | 0 | 8 | 70 | 22 | 0 | 5 | 71 | 24 | 0 |
| RevBayes | 1 | 6 | 88 | 5 | 2 | 22 | 71 | 5 | 1 | 23 | 76 | 0 |
| IQ-TREE | 86 | 11 | 3 | 0 | 90 | 8 | 2 | 0 | 94 | 6 | 0 | 0 |
| RAxML | 0 | 0 | 5 | 95 | 0 | 0 | 5 | 95 | 0 | 0 | 0 | 100 |

Supplementary Table S7: Results of the rank test using the KF values for each data set replicate. Phylogenetic inference programs were ranked from the best (1st rank) to the worst performing (4th rank) based on the accuracy of the reconstructed topologies. Numbers indicate percentage of the total number of analyses in which programs scored at each rank.

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|  | **0% missing data** | | | | **20% missing data** | | | | **50% missing data** | | | |
| **1** | **2** | **3** | **4** | **1** | **2** | **3** | **4** | **1** | **2** | **3** | **4** |
| MrBayes | 0 | 46 | 26 | 28 | 0 | 35 | 33 | 32 | 28 | 72 | 0 | 0 |
| RevBayes | 0 | 31 | 1 | 68 | 9 | 22 | 15 | 54 | 0 | 0 | 3 | 97 |
| IQ-TREE | 0 | 23 | 73 | 4 | 0 | 34 | 52 | 14 | 72 | 28 | 0 | 0 |
| RAxML | 100 | 0 | 0 | 0 | 91 | 9 | 0 | 0 | 0 | 0 | 97 | 3 |